REMARKS

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §§1.821(e), (f) and (g), or §§1.825(d) and (b), respectively, are the same, and that the attached sequence listing and computer readable form copy contain no new matter. A copy of the "Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures" is also enclosed.

Applicant does not believe there are any fees required for the submission of this sequence listing. However, the Commissioner is authorized to charge Lyon & Lyon's Deposit Account No. **12-2475** for any fees required and to credit any overpayments to said Deposit Account **12-2475**.

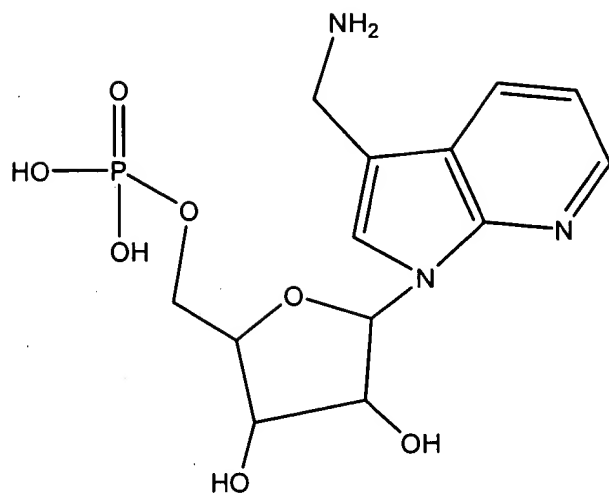Respectfully submitted,

LYON & LYON LLP

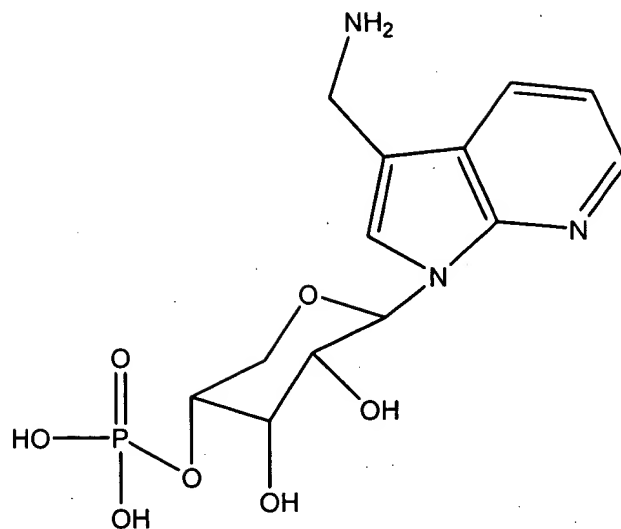Dated: <u>August 9, 2001</u>

By: _____
Patrick S. Eagleman
Reg. No. 44,665

633 West Fifth Street, Suite 4700
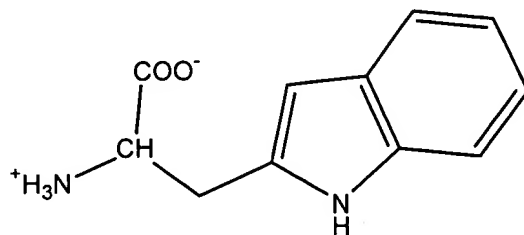Los Angeles, California 90071-2066
(213) 489-1600

ILLUSTRATIONS

Tryptamine furanosyl nucleoside
(RNA)

Tryptamine pyranosyl nucleoside
(p-RNA)

Tryptophan
(Amino Acid)

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/374.3`8	06/13/99	HELLER	M 241/172

```
023243
LYON & LYON LLP                        HM12/1001
633 WEST FIFTH STREET
SUITE 4700
LOS ANGELES CA 90071
```

EXAMINER
PRASTHOFER, T

ART UNIT	PAPER NUMBER
1627	14

DATE MAILED: 10/01/01

atty: DBM - oc
P. Eagleman - oc

cc: RNS
RWO
Alma

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner, of Patents and Trademarks

PTO-90C (Rev.11/00)
*U.S. GPO: 2000-475-249/45175

2 - Mail Copy

	Application No.	Applicant(s)
Notice of Abandonment	09/374,338	HELLER ET AL.
	Examiner	**Art Unit**
	Thomas W Prasthofer	1627

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

This application is abandoned in view of:

1. ☒ Applicant's failure to timely file a proper reply to the Office letter mailed on *24 July 2001*.

   (a) ☐ A reply was received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the period for reply (including a total extension of time of _____ month(s)) which expired on _____.

   (b) ☐ A proposed reply was received on _____, but it does not constitute a proper reply under 37 CRF 1.113 (a) to the final rejection.

     (A proper reply under 37 CRF 1.113 to a final rejection consists only of: (1) a timely filed amendment which places the application in condition for allowance; (2) a timely filed Notice of Appeal (with appeal fee); or (3) a timely filed Request for Continued Examination (RCE) in compliance with 37 CFR 1.114).

   (c) ☐ No reply has been received.

2. ☐ Applicant's failure to timely pay the required issue fee and publication fee, if applicable, within the statutory period of three months from the mailing date of the Notice of Allowance (PTOL-85).

   (a) ☐ The issue fee and publication fee, if applicable, was received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the statutory period for payment of the issue fee (and publication fee) set in the Notice of Allowance.

   (b) ☐ The submitted fee of $_____ is insufficient. A balance of $_____ is due.

     The issue fee required by 37 CFR 1.18 is $_____. The publication fee, if required by 37 CFR 1.18(d), is $_____.

   (c) ☐ The issue fee and publication fee, if applicable, has not been received.

3. ☐ Applicant's failure to timely file new formal drawings as required by, and within the three-month period set in, the Notice of Allowability (PTO-37).

   (a) ☐ Proposed new formal drawings were received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the period for reply.

   (b) ☐ The proposed new formal drawings filed on _____ are not acceptable and the period for reply has expired.

   (c) ☐ No proposed new formal drawings have been received.

4. ☐ The letter of express abandonment which is signed by the attorney or agent of record, the assignee of the entire interest, or all of the applicants.

5. ☐ The letter of express abandonment which is signed by an attorney or agent (acting in a representative capacity under 37 CFR 1.34(a)) upon the filing of a continuing application.

6. ☐ The decision by the Board of Patent Appeals and Interference rendered on _____ and because the period for seeking court review of the decision has expired and there are no allowed claims.

7. ☒ The reason(s) below:

   Applicant's response to the comunication mailed July 24, 2001 (Non-Bona Fide attempt to comply with the sequence rules) did not comply with the sequence rules, 37 C.F.R. 1.136. The application is abandoned under 37 C.F.R. 1.821(g). A copy of the sequenc elisting error report is attached.

DR. JYOTHSNA VENKAT PH.D
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

U.S. Patent and Trademark Office
PTO-1432 (Rev. 9-00)

Notice of Abandonment

Part of Paper No. 14

EXHIBIT "B"
Page 2 of 10

T. PRAST OFFER
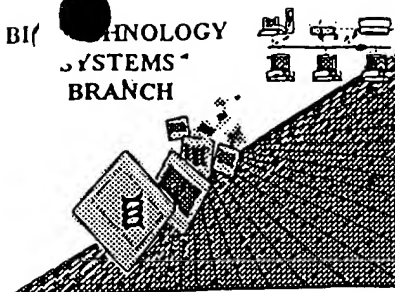
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _____ 09/374 338 B _____

Source: _____ CIPE. _____

Date Processed by STIC: _____ 08/23/2001 _____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
    APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
    NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/374 338 B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
    Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
    Numbering

The numbering under each 5* amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length.

Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
    "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
    (OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
    (NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
    (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _✓_ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 08/23/2001
PATENT APPLICATION: US/09/374,338B TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

```
 3 <110> APPLICANT: Heller, Michael J.
 4         Windhab, Norbert
 5         Anderson, Richard R.
 6         Ackley, Donald E.
 7         Nova, Tina S.
 8         Hoppe, Hans-Ullrich
 9         Hamon, Christian
11 <120> TITLE OF INVENTION: MICROELECTRONIC MOLECULAR DESCRIPTOR ARRAY DEVICES, METHODS,
PROCEDURES,
12         AND FORMATS FOR COMBINATORIAL SELECTION OF INTERMOLECULAR LIGAND BINDING
13         STRUCTURES AND FOR DRUG SCREENING
15 <130> FILE REFERENCE: Patrick Eagleman: Nanogen 241/172
17 <140> CURRENT APPLICATION NUMBER: 09/374,338B
18 <141> CURRENT FILING DATE: 1999-08-13
20 <160> NUMBER OF SEQ ID NOS: 31
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 7
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Synthetic test construct
32 <220> FEATURE:
33 <221> NAME/KEY: modified_base
34 <222> LOCATION: (1)..(7)
35 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
38 <220> FEATURE:
39 <221> NAME/KEY: modified_base
40 <222> LOCATION: (1)..(1)
41 <223> OTHER INFORMATION: Base 1 is tryptamine
44 <220> FEATURE:
45 <221> NAME/KEY: modified_base
46 <222> LOCATION: (7)..(7)
47 <223> OTHER INFORMATION: Base 7 is modified with Texas Red
50 <400> SEQUENCE: 1
51 ngaaggg
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 14
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic test construct
62 <220> FEATURE:
63 <221> NAME/KEY: modified_base
64 <222> LOCATION: (1)..(14)
65 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
68 <220> FEATURE:
69 <221> NAME/KEY: modified_base
```

W--> (handwritten marker by line 51)

Handwritten notes:

Does Not Comply
Corrected Diskette Needed

n can only represent a single nucleotide base at any single location.

FYI - tryptamine is an amino acid or protein

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

```
 70 <222> LOCATION: (1)..(1)
 71 <223> OTHER INFORMATION: Base 1 is modified with Biotin
 74 <220> FEATURE:
 75 <221> NAME/KEY: modified_base
 76 <222> LOCATION: (8)..(8)
 77 <223> OTHER INFORMATION: Base 8 is tryptamine
 80 <400> SEQUENCE: 2
 81 cccttctncc cccg
 84 <210> SEQ ID NO: 3
 85 <211> LENGTH: 7
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: Synthetic test construct
 93 <220> FEATURE:
 94 <221> NAME/KEY: modified_base
 95 <222> LOCATION: (1)..(7)
 96 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
 99 <220> FEATURE:
100 <221> NAME/KEY: modified_base
101 <222> LOCATION: (1)..(1)
102 <223> OTHER INFORMATION: Base 1 is modified with Cyanine-3 flourescent dye
105 <220> FEATURE:
106 <221> NAME/KEY: modified_base
107 <222> LOCATION: (7)..(7)
108 <223> OTHER INFORMATION: Base 7 is tryptamine
111 <400> SEQUENCE: 3
112 cgggggn
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 7
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Synthetic test construct
124 <220> FEATURE:
125 <221> NAME/KEY: modified_base
126 <222> LOCATION: (1)..(7)
127 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
130 <220> FEATURE:
131 <221> NAME/KEY: modified_base
132 <222> LOCATION: (3)..(3)
133 <223> OTHER INFORMATION: Base 3 is tryptamine
136 <220> FEATURE:
137 <221> NAME/KEY: modified_base
138 <222> LOCATION: (4)..(4)
139 <223> OTHER INFORMATION: Base 4 is tryptamine
142 <220> FEATURE:
143 <221> NAME/KEY: modified_base
144 <222> LOCATION: (5)..(5)
```

W--> 81

W--> 112 Errored

[handwritten annotations:]

n can only represent a single nucleotide base at any single location.

n can only represent a single nucleotide base at any single location

FYI tryptamine is an amino acid

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

```
        145 <223> OTHER INFORMATION: Base 5 is tryptamine
        148 <400> SEQUENCE: 4
W-->  149 ccnnngg                                                    7
       152 <210> SEQ ID NO: 5
        153 <211> LENGTH: 7
        154 <212> TYPE: DNA
        155 <213> ORGANISM: Artificial Sequence
        157 <220> FEATURE:
        158 <223> OTHER INFORMATION: Synthetic test construct
        161 <220> FEATURE:
        162 <221> NAME/KEY: modified_base
        163 <222> LOCATION: (1)..(7)
        164 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
        167 <220> FEATURE:
        168 <221> NAME/KEY: modified_base
        169 <222> LOCATION: (1)..(1)
        170 <223> OTHER INFORMATION: Base 1 modified with Fluorophore
        173 <220> FEATURE:
        174 <221> NAME/KEY: modified_base
        175 <222> LOCATION: (7)..(7)
        176 <223> OTHER INFORMATION: Base 7 modified with a Peptide
        179 <220> FEATURE:
        180 <221> NAME/KEY: modified_base
        181 <222> LOCATION: (7)..(7)     Errored
        182 <223> OTHER INFORMATION: Base 7 is tryptamine
        185 <400> SEQUENCE: 5
W-->  186 cgggggh                                                    7
        189 <210> SEQ ID NO: 6
        190 <211> LENGTH: 8
        191 <212> TYPE: DNA
        192 <213> ORGANISM: Artificial Sequence
        194 <220> FEATURE:
        195 <223> OTHER INFORMATION: Synthetic test construct
        198 <220> FEATURE:
        199 <221> NAME/KEY: modified_base
        200 <222> LOCATION: (1)..(8)
        201 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
        204 <220> FEATURE:
        205 <221> NAME/KEY: modified_base
        206 <222> LOCATION: (1)..(1)
        207 <223> OTHER INFORMATION: Base 1 modified with a Peptide
        210 <220> FEATURE:
        211 <221> NAME/KEY: modified_base     Errored
        212 <222> LOCATION: (1)..(1)
        213 <223> OTHER INFORMATION: Base 1 is tryptamine
        216 <220> FEATURE:
        217 <221> NAME/KEY: modified_base
        218 <222> LOCATION: (8)..(8)
        219 <223> OTHER INFORMATION: Base 8 is any nucleotide  OK
```

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W--> 223 hgaagggh
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      227 <211> LENGTH: 14
      228 <212> TYPE: DNA
      229 <213> ORGANISM: Artificial Sequence
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      232 <223> OTHER INFORMATION: Synthetic test construct
      235 <220> FEATURE:
      236 <221> NAME/KEY: modified_base
      237 <222> LOCATION: (1)..(14)
      238 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
      241 <220> FEATURE:
      242 <221> NAME/KEY: modified_base
      243 <222> LOCATION: (1)..(1)
      244 <223> OTHER INFORMATION: Base 1 modified with Biotin
      247 <220> FEATURE:
      248 <221> NAME/KEY: modified_base
      249 <222> LOCATION: (7)..(7)
      250 <223> OTHER INFORMATION: Base 7 is tryptamine
      253 <220> FEATURE:
      254 <221> NAME/KEY: modified_base
      255 <222> LOCATION: (7)..(8)
      256 <223> OTHER INFORMATION: Bases 7 and 8 are modified by Peptide connection.
      259 <400> SEQUENCE: 7                                                         14
W--> 260 ccccttcntcc cccg
      263 <210> SEQ ID NO: 8
      264 <211> LENGTH: 6
      265 <212> TYPE: PRT
      266 <213> ORGANISM: Artificial Sequence
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      269 <223> OTHER INFORMATION: Synthetic test construct
      272 <220> FEATURE:
      273 <221> NAME/KEY: PEPTIDE
      274 <222> LOCATION: (1)..(1)
      275 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
      278 <400> SEQUENCE: 8
      280 Cys Leu Ser Leu Glu Gly
      281 1               5
      283 <210> SEQ ID NO: 9
      284 <211> LENGTH: 6
      285 <212> TYPE: PRT
      286 <213> ORGANISM: Artificial Sequence
      288 <220> FEATURE:
      289 <223> OTHER INFORMATION: Synthetic test construct
      292 <220> FEATURE:
      293 <221> NAME/KEY: PEPTIDE
      294 <222> LOCATION: (1)..(1)
      295 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
```

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

```
298 <400> SEQUENCE: 9
300 Cys Ser Leu Glu Ser Gly
301 1               5
303 <210> SEQ ID NO: 10
304 <211> LENGTH: 6
305 <212> TYPE: PRT
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic test construct
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313 <221> NAME/KEY: PEPTIDE
314 <222> LOCATION: (1)..(1)
315 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
318 <400> SEQUENCE: 10
320 Cys Leu Leu Ser Glu Gly
321 1               5
323 <210> SEQ ID NO: 11
324 <211> LENGTH: 6
325 <212> TYPE: PRT
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Synthetic test construct
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333 <221> NAME/KEY: PEPTIDE
334 <222> LOCATION: (1)..(1)
335 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
338 <400> SEQUENCE: 11
340 Cys Ser Arg Ser Arg Gly
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343 <210> SEQ ID NO: 12
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345 <212> TYPE: PRT
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349 <223> OTHER INFORMATION: Synthetic test construct
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354 <222> LOCATION: (1)..(1)
355 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
358 <400> SEQUENCE: 12
360 Cys Ser Arg His Arg Gly
361 1               5
363 <210> SEQ ID NO: 13
364 <211> LENGTH: 6
365 <212> TYPE: PRT
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: Synthetic test construct
372 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 08/23/2001
PATENT APPLICATION: US/09/374,338B   TIME: 13:24:32

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

```
L:51  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:81  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
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L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
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